WEST

Generate Collection

L4: Entry 1 of 10 File: USPT Apr 10, 2001

DOCUMENT-IDENTIFIER: US 6214551 B1
TITLE: Oligonucleoside linkages containing adjacent nitrogen atoms

DEPR:
The dimeric oligonucleoside 58 will be utilized as building block units in a conventional oligonucleotide solid support synthesis as per the procedure of Example 80. For the purpose of illustration a polymer incorporating seven nucleosides is described. A first unit of the dimeric oligonucleoside 58 will be coupled to a first cytidine nucleoside tethered to a solid support via its 3' hydroxyl group and having a free 5' hydroxyl group. After attachment of the first unit of compound 58 to the support, the 5'-dimethoxytrityl group of that first compound 58 unit will be removed in the normal manner. A second compound 58 unit will then be coupled via its .beta.-cyanoethyl-N-diisopropylphosphiryl group to the first compound 58 unit using normal phosphoramidate chemistry. This forms a conventional phosphodiester bond between the first and second compound 58 units and elongates the polymer by two nucleosides (or one oligonucleoside dimer unit). The dimethoxytrityl blocking group from the second compound 58 unit will be removed in the normal manner and the polymer elongated by a further dimeric unit of compound 58. As with addition of the first and second dimeric units, the third unit of compound 58 is coupled to the second via conventional phosphoramidite procedures. The addition of the third unit of compound 58 completes the desired length and base sequence. This polymer has a backbone of alternating normal phosphodiester linkages and the methyl-(iminooxymethylene) linkages of compound 58. The 5' terminal dimethoxytrityl group of the third compound 58 unit will be removed in the normal manner followed by release of the polymer from the solid support, also in the normal manner. Purification of the polymer will be achieved by HPLC to yield compound 91 wherein, utilizing the structure of Scheme XVI, T.sub.3 and T.sub.5 are OH, D is O, E is OH, X is H, Q is O, r is 1 and for the seven nucleoside polymer described, q is 3; and for each q, i.e., q.sub.1, q.sub.2 and q.sub.3, n and p are 1 in each instances; and for q, and q.sub.2, m is 1; and for q.sub.3, m is 0; and Bxk is cytosine; and each BxJ and Bxi is thymine.

WEST

Generate Collection

L1: Entry 1 of 27 File: USPT Oct 9, 2001

DOCUMENT-IDENTIFIER: US 6300076 B1
TITLE: DNA diagnostics based on mass spectrometry

DEPR:
The schematic presentation as given in FIG. 34 shows the expected short sequencing products with the theoretically calculated molecular mass of the wildtype and various mutations of exon 10 of the CFTR-gene. The short sequencing products were produced using either ddTTP (FIG. 34A) or ddCTP (FIG. 34B) to introduce a definitive sequence related stop in the nascent DNA strand. The MALDI-TOF-MS spectra of healthy, mutation heterozygous, and mutation homozygous individuals are presented in FIG. 35. All samples were confirmed by standard Sanger sequencing which showed no discrepancy in comparison to the mass spec analysis. The accuracy of the experimental measurements of the various molecular masses was within a range of minus 21.8 and plus 87.1 dalton (Da) to the range expected. This is a definitive interpretation of the results allowed in each case. A further advantage of this procedure is the unambiguous detection of the .DELTA.I507 mutation. In the ddTTP reaction, the wildtype allele would be detected, whereas in the ddCTP reaction the three base pair deletion would be disclosed.

6268144
6221601
6043031

WEST

Generate Collection

L1: Entry 25 of 27 File: USPT Aug 20, 1996

DOCUMENT-IDENTIFIER: US 5547835 A
TITLE: DNA sequencing by mass spectrometry

DEPR:
As used herein, the superscript 0-i designates i+1 mass differentiated nucleotides, primers or tags. In some instances, the superscript 0 (e.g., NTP.sup.0, UP.sup.0) can designate an unmodified species of a particular reactant, and the superscript i (e.g., NTP.sup.i, NTP.sup.1, NTP.sup.2, etc.) can designate the i-th mass-modified species of that reactant. If, for example, more than one species of nucleic acids (e.g., DNA clones) are to be concurrently sequenced by multiplex DNA sequencing, then i+1 different mass-modified nucleic acid primers (UP.sup.0, UP.sup.1, . . . UP.sup.i) can be used to distinguish each set of base-specifically terminated fragments, wherein each species of mass-modified UP.sup.i can be distinguished by mass spectrometry from the rest.